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15949 U.S. PTO

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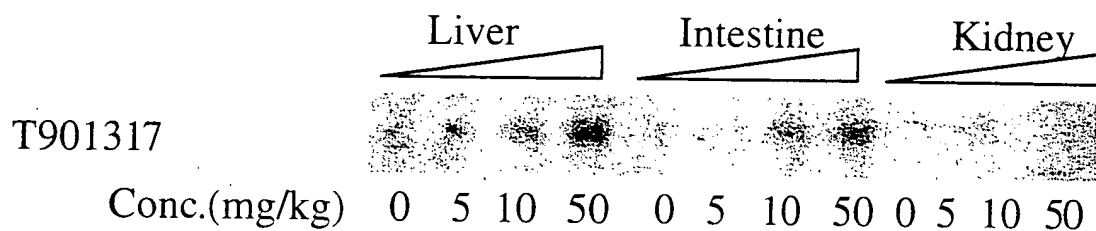
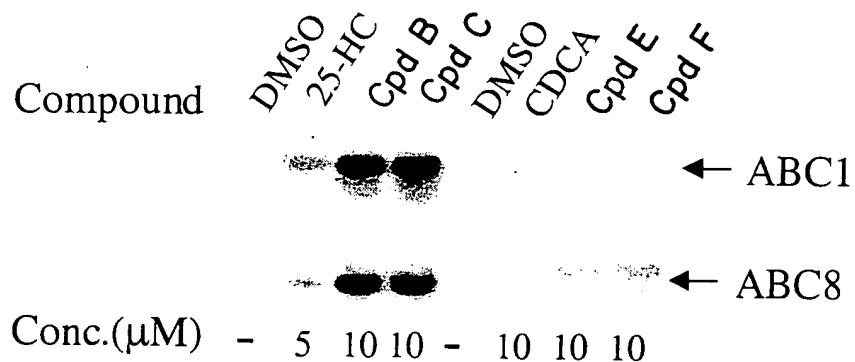


FIG. 1.



LXR agonist: Cpd B, C

FXR agonist: Cpd E, F

FIG. 2.

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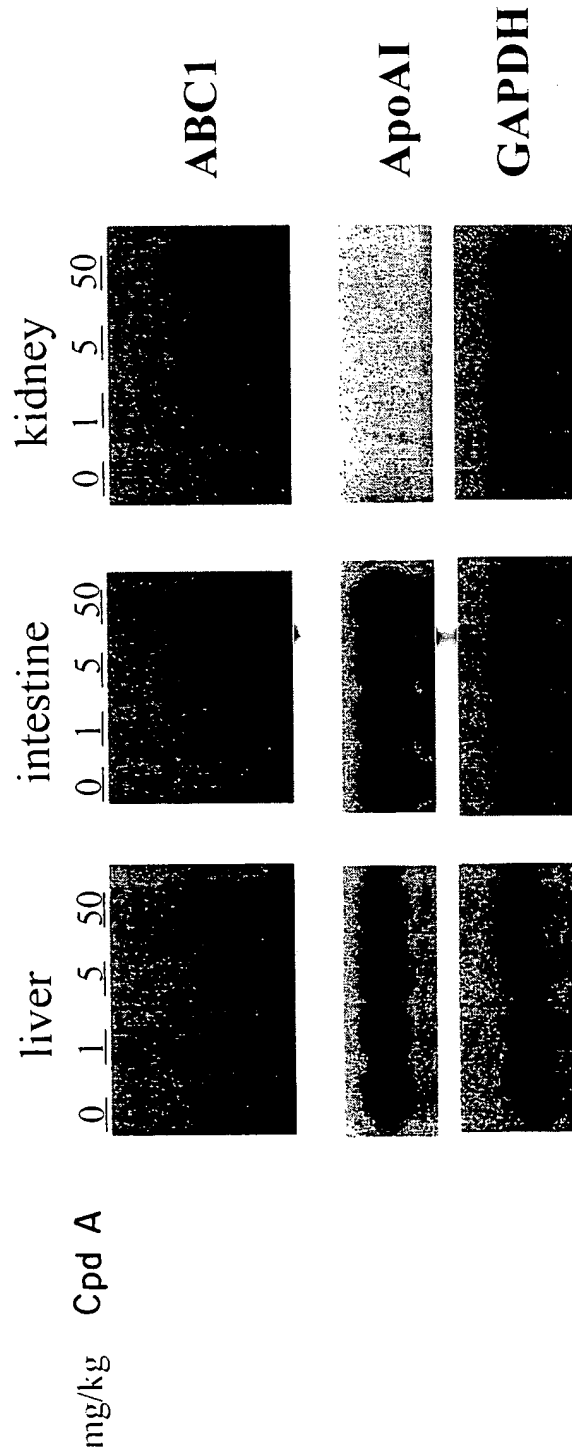


FIG. 3.

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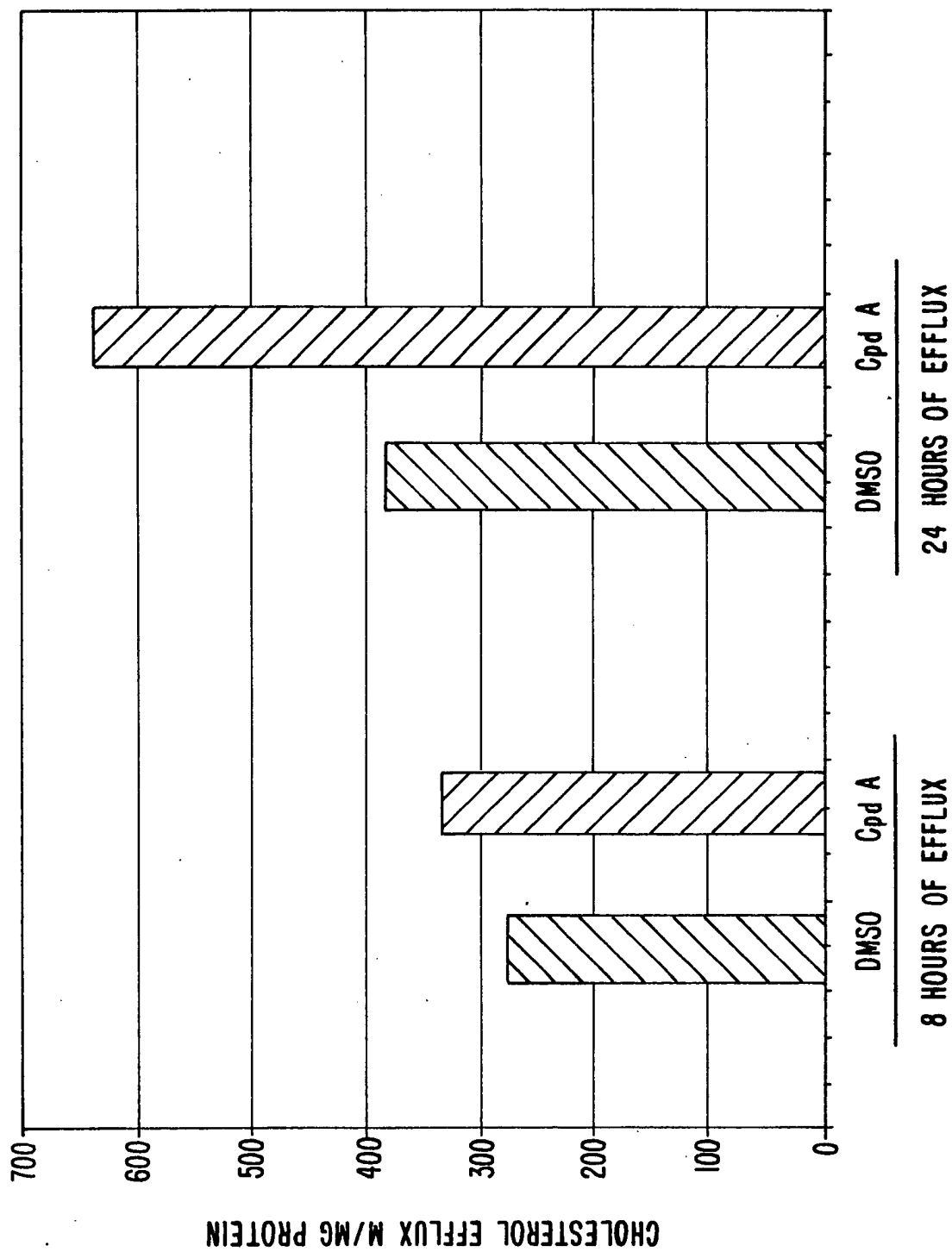


FIG. 4.

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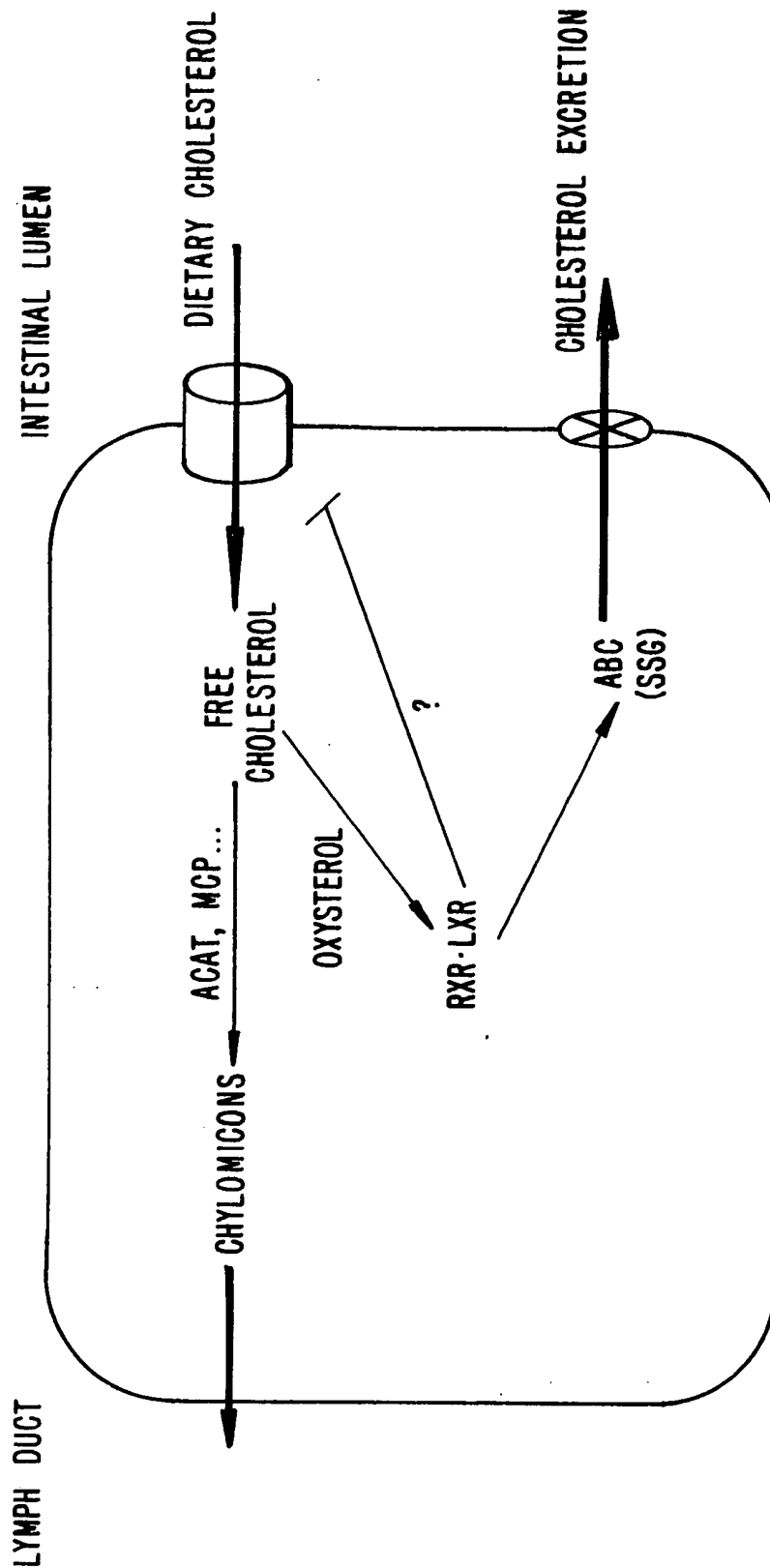
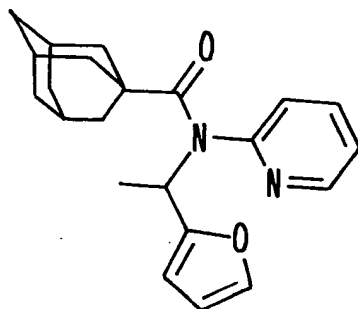


FIG. 5.

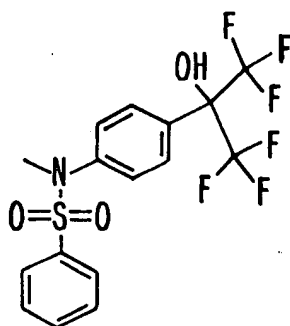
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COMPOUND C



COMPOUND B



COMPOUND A

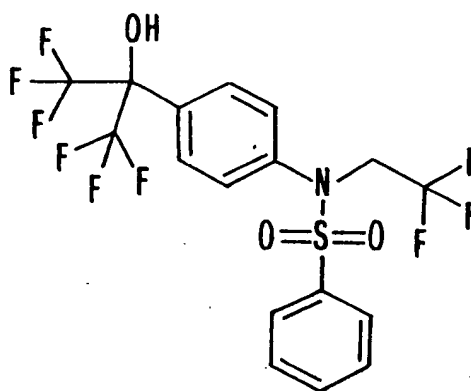


FIG. 6.

ACAGGCCACTAGAAAATTCACCTTGCAATTGCTTCCCTGCTAGCCATGGGTGAGCTGCCCTTTCTGAGTCCAGAGGGAGCCAGAGGGCCTCACA 95
M G E L P F L S P E G A R G P H
ACAGAGGCTCTGAGCTCCCTGGAGCAAGTTTCGGTCACGGGCACAGAGGCTCGGCACAGCTTAGGTGTCTCCTGACATGTGTCTACAGCGTC 190
N R G S L S L E Q G S V T G T E A R H S L G V L H V S Y S V
AACCGTGTGGGCCCTTGGTGAACATCAAAATCATGCCAGCAGAAGTGGACAGGCAAATCCTCAAAGATGTCTCCTTGTACATCGAGAGTGG 285
N R V G P W N I K S C Q Q K W D R Q I L K D V S L V I E S G
GATTATGTGCATCTTAGGCAGCTCAGGCTCAGGGAAGACACGCTGCTGGACGCCATCTCCGGGAGGCTGCGGCGCACTGGGACCCCTGGAAG 380
I M C I L G S S G S G K T T L L D A I S G R L R R T G T L E
AGGTGTTTGTGAATGGCTGCGAGCTGCGCAGGACCAAGTCCCAAGACTGCTTCTCCTACGTCTGACAGCGACGTTTCTTGAGCAGCCTC 475
E V F V N G C E L R R D Q F Q D C F S Y V L Q S D V F L S S L
GTGCGGAGACGTTGCGATACACAGCGATGCTGGCCCTCTGCGCGAGCTCCGCGGACTTCTACAAACAAGAAGGTAGAGGCAGTCATGACAGA 570
V R E T L R Y T A M L A L C R S S A D F Y N K K V E A V M T E
GAGCCTGAGCCACGTGGCGGACCAAAATGATTGGGAGCTATAATTTTGGGGAATTTCCAGTGGCGAGCGGCGCGAGTTTCCATCGCAGCCCC 665
S L S H V A D Q M I G S Y N F G G I S S G E R R R V S I A A
TCCTTCAGGACCCCAAGTCATGCTAGATGAGCCCAACACAGGACTGGACTGCATGACTGCAAAATCAAATGTCTCTTCTTGCTGAG 760
L L Q D P K V M L D E P T T G L D C M T A N Q I V L L L A E
GCTCGCAGGGACCGAATTGTGATTGTACCATCCACCGCTCGCTCTGAGCTCTTCCAACACTTCGACAAAAATTGCCATCCTGACTTACGG 855
A R R D R I V I V T I H Q P R S E L F Q H F D K I A I L T Y G
GTTGGTGTCTGTGGCACCCTGAGGAGATGCTTGGCTTCTTCAATAACTGTGGTTACCCCTGTCTCTGAACATTCCAATCCCTTTGATTTT 950
L V F C G T P E E M L G F F N N C G Y P C P E H S N P F D F
TGGAATGACATCAGTGGACACCCCAAGCAGAGCGGGAAATAGAAACGTACAAGCGAGTACAGATGCTGGAATGTGCCTTCAAGGAATCT 1045
M D L T S V D T Q S R E R E I E T Y K R V Q M L E C A F K E S

FIG. 7A.

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ATCTATCACAAAATTCTGGAGAACATTGAAAGAGCACGATACCTGAAACCTTACCCATGGTTCCCTTTCAAAAACAAAAGATCCTCCTGGGAT 1140
I Y H K I L E N I E R A R Y L K T L P M V P F K T K D P P G M
CGGCAAGCTTGGTGTCTCTGAGCGAGTAACAAGAACTTAATGAGGAATAAGCAGGCAGTGATTATGCGTCTCGTTTCAGAAATCTGATCA 1235
G K L G V L L R R V T R N L M R N K Q A V I M R L V Q N L I
GCCTCTTCTCATTTTCTACCTTCTCCGCGTCCAGAACACACGCTAAAGGGCGCTGTGCAGGACCGCGTGGGGCTGCTCTATCAGCTTGTG 1330
G L F L I F Y L L R V Q N N T L K G A V Q D R V G L L Y Q L V
GCCACCCCATACACCGGCATGCTCAATGCTGTGAATCTGTTCCTCATGCTGAGAGCCGTCAGCGACCAAGAGAGTCAGGATGGCCTGTATCA 1425
A T P Y T G M L N A V N L F P M L R A V S D Q E S Q D G L Y H
GTGGCAGATGCTGCTCGCCTACGTGCTACACGTCCTCCCTTCAGCGTCATCGCCACGGTCATTTTCAGCAGTGTGTATTGGACTCTGG 1520
W Q M L L A Y V L H V L P F S V I A T V I F S S V C Y W T L
TGATATCCTGAAGTTGCCAGATTGGATATTCTCTGCTGCTCTTTTGGCCCCCTCACTTAATTGGAGAAATTTCTAACACTTGTGCTGTGGT 1615
L Y P E V A R F G Y F S A A L L A P H L I G E F L T L V L L G
GTCCAAAACCCCTAATATGTCAACAGTATAGTGGCTCTGCTCAGCATCTCTGGGCTGCTTATTGGATCTGGATTATCAGAAACATACAAGA 1710
V Q N P N I V N S I V A L L S I S G L L I G S G F I R N I Q E
GCCCATTCCCTTTAAAAATCCTGGGTTATTTTACATTCCAAAAATACTGTTGTGAGATTCTCGTGGTCAATGAGTTTACGGCCTGAACTTCA 1805
P I P L K I L G Y F T F Q K Y C C E I L V V N E F Y G L N F
GTGGTGGATCCAACACCTCTATGCTAAATCACCCGATGTGCGCCATCACCCCAAGGGTCCAGTTCATCGAGAAAACCTGCCCAGGTGCTACA 1900
C G G S N T S M L N H P M C A I T Q G V Q F I E K T C P G A T
AGATTACGGCAAACCTTCCTCATCTTATATGGGTTTATCCAGCTCTGGTCATCCTAGGAATAGTGATTTTAAAGTCAGGGACTACCTGAT 1995
R F T A N F L I L Y G F I P A L V I L G I V I F K V R D Y L I
CAGATAGTTAAGATGACAGGCAGGAAAGGGTTAATGGGCAGGCACGCCCTGCTGGAGCACAGAGAAGTACTGTCTTCAACCATCAGGATC 2090
R X>

FIG. 7B.

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CTGGACCCCTTGTTCTATCCGGAGCCCCAAGGGCAACGAGAACTCACAGCCCTCTGCTATTCCAGCTTGTTGGGCAAT 2185
GTGCTTGGACATTGTGACTGACTGCAATAATGTAATAATAATAATTCATAAACCTACAGGACATT 2258

FIG. 7C.

AGGTGAGCAGGCGAGTCTGCCACGGGCTCCCCAACTGAAGCCACTCTGGGGAGGGTCCGGCCACCAGAAAATTGCCCCAGCTTTGCT 95
TGTGGCCATGGGTGACCTCTCATCTTTGACCCCCGGAGGGTCCATGGGTCTCCAAGTAAACAGAGGCTCCAGAGCTCCCTGGAGGGGCT 190
M G D L S S L T P G G S M G L Q V N R G S Q S S L E G A
GCCACCGCCCCGGAGCCTCACAGCCTGGGCATCCTCCATGCCCTACAGCGTCAGCCACCGCGTGAGGCCCTGGTGGACATCACATCTTG 285
A T A P E P H S L G I L H A S Y S V S H R V R P W D I T S C
GCAGAGTGGACCGCAGATCCTCAAAGATGTCTCCTTGTACGTGGAGAGCGGGCAGATCATGTGCATCCTAGGAAGCTCAGGCTCCGGGA 380
Q Q W T R Q I L K D V S L Y V E S G Q I M C I L G S S G S G
CCACGCTGCTGACGCCATGTCCGGAGGCTGGGCGCGCGGGACCTTCCTGGGGAGGTGTATGTGAACGGCCGGCGCTGCCGCCGGGAG 475
T T L L D A M S G R L G R A G T F L G E V Y V N G R A L R R E
TTCAGGACTGCTTCTCCTACGTCTGCAGAGCGACACCCCTGCTGAGCAGCCTCACCGTGCGCGAGACGCTGCACACCGCGCTGCTGGC 570
F Q D C F S Y V L Q S D T L L S S L T V R E T L H Y T A L L A
CCGCCGGGCAATCCCGGCTCCTCCAGAAGAAGGTGGAGGCCGTCATGGCAGAGCTGAGTCTGAGCCATGTGGCAGACCGACTGATTGGCA 665
R R G N P G S F Q K K V E A V M A E L S L S H V A D R L I G
ACAGCTTGGGGGCATTTCACGGGTGAGCGCGCGGGTCTCCATCGCAGCCCCAGCTGCTCCAGGATCCTAAGTGCATGCTGTTGATGAG 760
Y S L G G I S T G E R R R V S I A A Q L L Q D P K V M L F D E
ACCACAGCCTGGACTGCTGCTAATCAGATTGTGCTCCTCCTGTTGGAAGTGGCTCGCAGGAACCGAATTGTGGTTCTCACCATTCA 855
T T B L D C M T A N Q I V V L L V E L A R R N R I V V L T I H

FIG. 8A.

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AGCCCCGTTCTGAGCTTTTTCAGCTCTTTTGACAAAATTGCCATCCTGAGCTTCGGAGAGCTGATTTTCTGTGGCAGCCAGCGGAAATGCTTG 950
P R S E L F Q L F Q L F D K I A I L S F G E L I F C G T P A E M L
TCTTCAATGACTGCGGTTACCCCTTGCTGAAACATTCAAACCCCTTTTGACTTCTATATGGACCTGACGTCAGTGGATACCCAAAGCAAGGAA 1045
F F N D C G Y P C P E H S N P F D F Y M D L T S V D T Q S K E
GAAATAGAAACCTCCAAGAGAGTCCAGATGATAGAATCTGCCTACAAGAAATCAGCAATTTGTCATAAACTTTGAAGAATATTGAAAGAAT 1140
E I E T S K R V Q M I E S A Y K K S A I C H K T L K N I E R M
ACACCTGAAAAACGTTACCAATGGTTCCCTTCAAAACCAAGATTTCTCCTGGAGTTTCTCTAAACTGGGTGTTCTCTCCTGAGGAGAGTGACAA 1235
H L K T L P M V P F K T K D S P G V F S K L G V L L R R V T
ACTTGGTGAGAAATAAGCTGGCAGTGATTACGCGTCTCCTTCAGAATCTGATCATGGGTTTGTTCCTCCTTTTCTCGTTCTCGGGTCCGA 1330
N L V R N K L A V I T R L L Q N L I M G L F L L F F V L R V R
AATGTGCTAAAGGTGCTATCCAGGACCGCGTAGGTCTCCTTTACCAGTTTGTGGGCGCCACCCCGTACACAGGCATGCTGAACGCTGTGAA 1425
N V L K G A I Q D R V G L L Y Q F V Q A T P Y T G M L N A V N
GTTTCCCGTGTGCGAGCTGTACGCGACCGAGAGTACGAGCGCCTCTACCAAGAGTGGCAGATGATGCTGGCCTATGCACTGCACGTCC 1520
F P V L R A V S D Q E S Q D G L Y Q K W Q M L A Y A L H V
CCTTCAGCGTTGTTGCCACCATGATTTTCAGCAGTGTGTGCTACTGGACGCTGGGCTTACATCCTGAGGTTGCCCGATTGGATATTTTCT 1615
P F S V V A T M I F S S V C Y W T L G L H P E V A R F G Y F S
GCTCTCTTGGCCCCCCTTAATTGGTGAATTTCTAACTCTTGTGCTACTTGGTATCGTCCAAAATCCAAATATAGTCAACAGTGTAGTGC 1710
A L L A P H L I G E F L T L V L L G I V Q N P N I V N S V V A
GCTGTCCATTGCGGGGGTGTGTTGGATCTGGATTCCCTCAGAAACATACAAGAAATGCCCATTCCTTTTAAATCATCAGTTATTTTACAT 1805
L S I A G V L V G S G F L R N I Q E M P I P F K I I S Y F T
AAAAATATTGCAGTGAGATTCTTGTAGTCAATGAGTTCTACGGACTGAATTTCACTTGTGGCAGCTCAAATGTTTCTGTGACAACTAATCCA 1900
Q K Y C S E I L V V N E F Y G L N F T C G S S N V S V T T N P

FIG. 8B.

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TGTGCCCTTCACTCAAGGAATTCAATTGAGAAAAACCTGCCCAGGTGCAACATCTAGATTCAACAATGAACTTTCTGATTTTGTATTCATT 1995
C A F T Q G I Q F I E K T C P G A T S R F T M N F L I L Y S F
TCCAGCTCTTGTCAATCCTAGGAATAGTTGTTTCAAAAATAAGGGATCATCTCATTTAGCAGGTAGTGAAAGCCATGGCTGGGAAAAATGGAAGT 2090
P A L V I L G I V V F K I R D H L I S R X>
GCTGCCGACTGTGCATGACTGCTCTGAACGCTCTGAAATGAGAGTGCCATGTATTTCTTTTGACAGGACATCTCAAGTCCTTTAACCATT 2185
CTCCATTGTGTCCTCTTGGATCCAAGCAGGCCCTTGAATGCAATGGAAAGTGGTTTATAGTCCCTTGCTCTTACAACCTGCAGGGACATGTGGT 2280
TTGGAAATTGTGACTGAGCGGACCCCAAGAATGTAAATAATATTCATAAACCTATGGG 2340

FIG. 8C.

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G.pro	MGDLSSLTTPG	GSMGLQVNRG	SOSSLEGAPA	TAPEP-HSLG	ILHASYSVSH	RVRPWWDITS	CROQWTRQIL	KDVSLEYV	ESG	79
G.pro	MGELPFLSEPE	GARGPHINRG	SLSSLEQGSV	TGTEARHSLG	VLHVSYSVN	RVGEPWNITKS	COQKMDRQIL	KDVSLEYV	ESG	80
G.pro	QIMCILGSSG	SGKTTLLDAM	SGRIGRAGTF	IGEVYVNGRA	LRREQFQDCF	SYVLQSDTLL	SSLTVRETLH	YTALLAIRRG	159	
G.pro	QIMCILGSSG	SGKTTLLDAI	SGRIRRTGTL	EGEVFNVCCE	LRRDQFQDCF	SYVLQSDVFL	SSLTVRETLR	YTAMLALCRS	160	
G.pro	NPGSFQKKVE	AVMAEELSLSH	VADRLLGNYS	IGGISTGERR	RVSIAAQLLQ	DPKVMLEFDEP	TTGLDCMTAN	QIVMLIVEELA	239	
G.pro	SADFYNNKKVE	AVMTELSLSH	VADQMIGSYN	EGGISSGERR	RVSIAAQLLQ	DPKVMLEFDEP	TTGLDCMTAN	QIVMLIVEELA	240	
G.pro	RNRIRIVLTI	HQPRSELFQI	FDKIAILSFG	ELIFCGTPAE	MIDFFNDCGY	PCPEHSNPF	FYMDLTSVDT	QSKEREIETS	319	
G.pro	RDRIRIVLTI	HQPRSELFQI	FDKIAILTYG	ELVFCGTTEE	MIGFFNDCGY	PCPEHSNPF	FYMDLTSVDT	QSKEREIETY	320	
G.pro	KRVQMIESAY	KKSAIICHKTL	KNIERMKHLK	TLPMVPFCTK	DSPGVFSKLG	VLLRRVTRNL	VRNKLAVITR	ILQNLIMGLF	399	
G.pro	KRVQMLECAF	KESDIYHKTL	ENIERARYLK	TLPMVPFCTK	DPPGMEGKLG	VLLRRVTRNL	MRNKQAVIMR	ILQNLIMGLF	400	
G.pro	ILIFVLRVRS	NVLKGAHQDR	VGLLYQFVGA	TPYTGMLNAV	NLFFMLRAVS	DQESQDGLYQ	KWQMLLAYAL	HVLPFSVAT	479	
G.pro	ILIFYLLRVQN	NTLKGAHQDR	VGLLYQFVGA	TPYTGMLNAV	NLFFMLRAVS	DQESQDGLYH	KWQMLLAYVL	HVLPFSVAT	480	
G.pro	MFSSVCYWT	LGLHPEVARF	GYFSAALLAP	HLIGEFLLTV	LLGIVQNPNI	VNSMVALLSI	AGMLVSGGFL	RNIQEMPIPF	559	
G.pro	VLFSVCYWT	LGLYPEVARF	GYFSAALLAP	HLIGEFLLTV	LLGIVQNPNI	VNSHVALLSI	SGILLGSGEI	RNIQEMPIPL	560	
G.pro	KIISYFTFQK	YCSEILVVNE	FYGLNFTCGS	SNVSVTTNPM	CAFTQGIQFI	EKTCPGATSR	FTMNFLLILYS	FIPALVILGI	639	
G.pro	KILGYFTFQK	YQCEILVVNE	FYGLNFTCGG	SNVSMLNHPM	CAFTQGVQFI	EKTCPGATSR	FTANFLILYG	FIPALVILGI	640	
G.pro	VVFRIIRDHLI	SR							651	
G.pro	VIFKVRDYLI	SR							652	

FIG. 9.

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Reference Number: 6711
Stanford RH Panel: TNG4
Lowest LDD Reported: 5
Chromosome Value: 0

Results for HT

Submitted

Vector:00010000000001000100001010010000000100000010001000
0000000010000000000001000000000001000100

SHGCNAME CHROM# LOD_SCORE DIST.(cRs)

1 SHGC-36672 2 7.52 35

Vector:00000000R00001010100100010011100000100000010001000
0000001010000000000001000000000R01000100

2 SHGC-8189 2 6.53 44

Vector:00000000100001010100100010011100000100000010001000
0000001010000000000001000000000101000100

3 SHGC-699 2 6.03 48

Vector:00010000000001000100001010010100100001000110001000
1000001010000000000000000100000011000100

The number of markers searched was 32440

FIG. 10.

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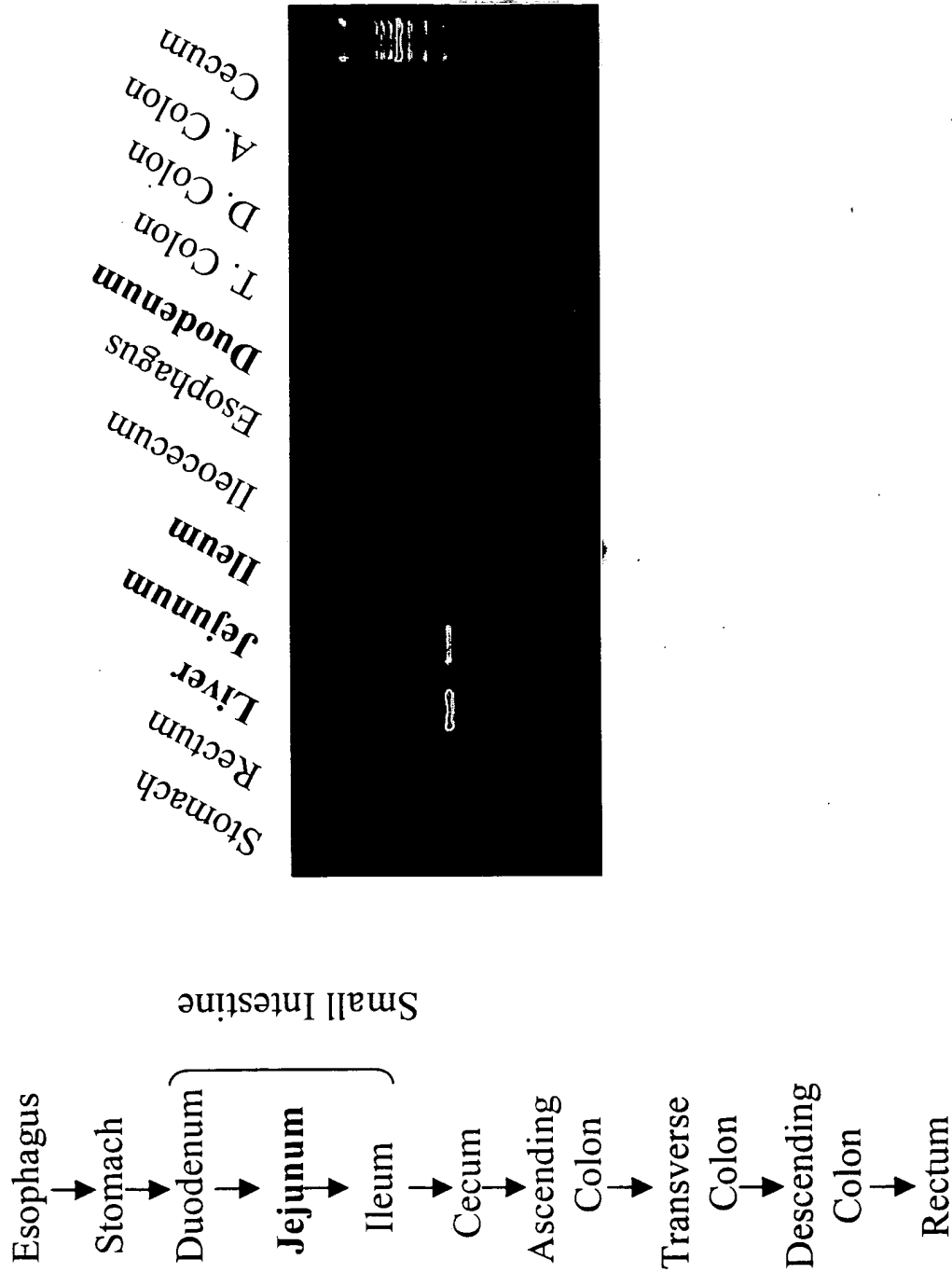


FIG. 11.

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Brain
Heart
Kidney
Liver
Lung
Pancreas
Placenta
S. Muscle
Colon
Ovary
PBL
Prostate
S. Intestine
Spleen
Testis
Thymus

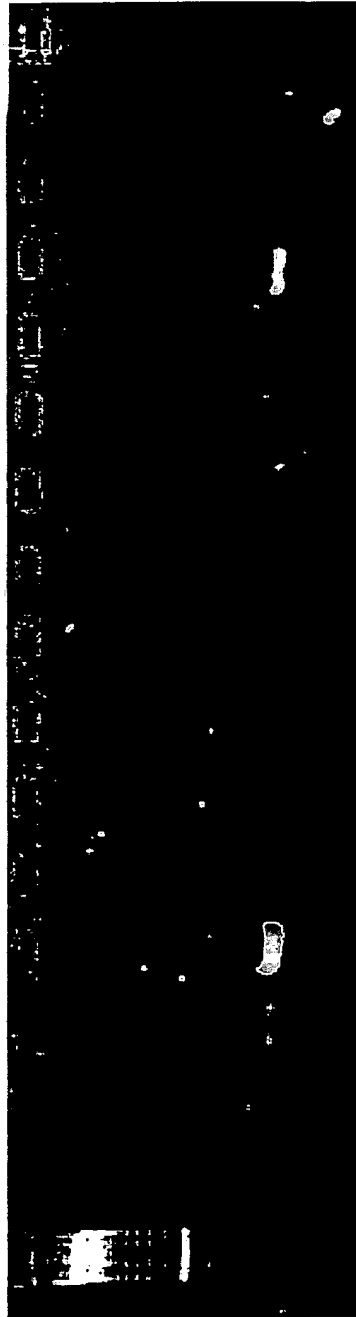


FIG. 12.

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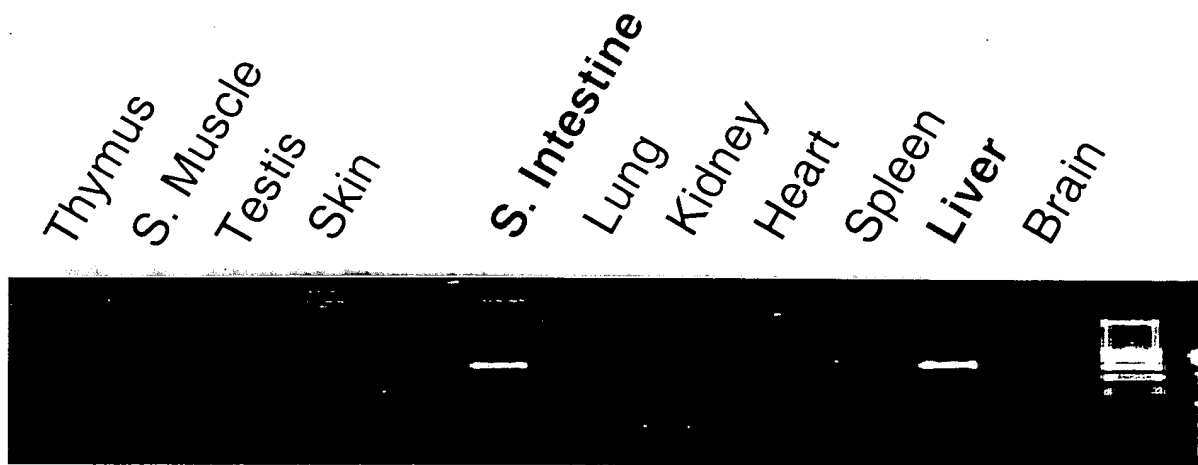


FIG. 13.

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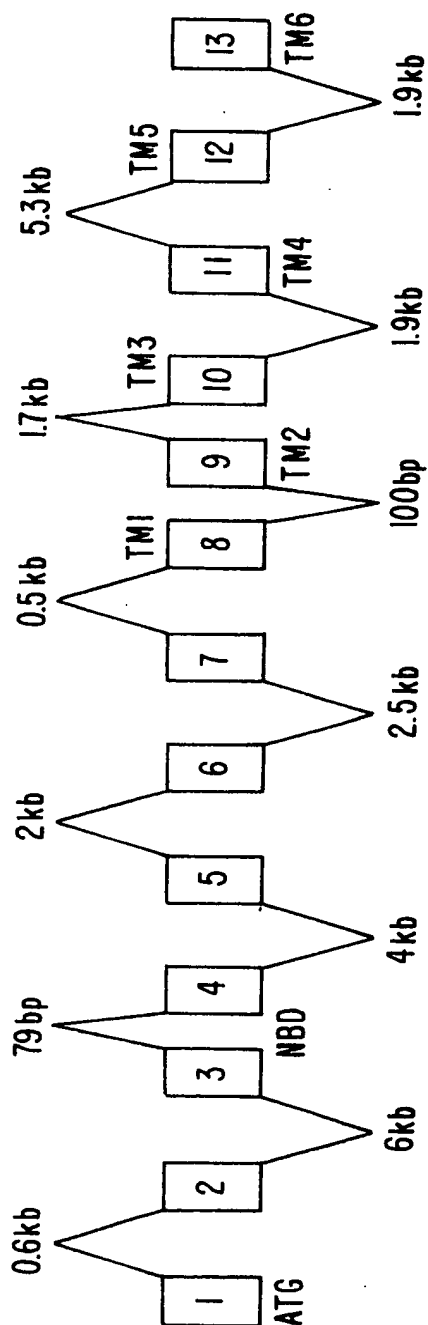


FIG. 14A.

AGGTGGAGCAGGCAGGCTGTGCCACGGGCTCCCCAACTGAAGCCACTCTGGGAGGGTCCGGCCACCAGAAAATTGCCCAGCTTTGCTGCCT
-----EXON 1-----
GGCCATGGGTGACCTCTCATCTTTGACCCCCGGAGGGTCCATGGGTCTCCAAGTAAACAGAGGCTCCCAGAGCTCCCTGGAGGGGGCTCCTGCCAC
-----EXON 1-----
CCCGAGCCTCACAGCCTGGCATCCTCCATGCCCTCCTACAGCGTCAGCCACCGCTGAGGCCCTGGTGGACATCACATCTTGCCGGCAGCAGTG
-----EXON 1-----
CAGGCAGATCCTCAAAGATGTCTCCTTGTACGTGGAGAGCGGGCAGATCATGTGCATCCTAGGAAGCTCAGGCTCCGGGAAAACACGCTGCTGGA
-----EXON 2-----
CATGTCCGGAGGCTGGGCGCGGGGACCTTCCTGGGGAGGTGTATGTGAACGGCCGGCGCTGCGCCGGGAGCAGTTCAGGACTGCTTCTC
-----EXON 3-----
CGTCTGCAGAGCGACACCCCTGCTGAGCAGCCTCACCGTGCAGAGACGCTGCACTACACCGCGCTGTGGCCATCCGCCGCGGCAATCCCGGCTC
-----EXON 3-----
CCAGAAGAAGGTGAGGCCGTGATGGCAGAGCTGAGTCTGAGCCATGTGGCAGACCGACTGATTGGCAACTACAGCTTGGGGGGCATTTCCACGGG
-----EXON 4-----
GCGGCGCCGGTCTCCATCGCAGCCAGCTGCTCAGGATCCTAAGGTGATGCTGTTGATGAGCCAAACACAGCCTGACTGCATGACTGCTAA
-----EXON 5-----
GATTGTCCTCCTGGTGGAACTGGCTCGCAGGAACCCGAATTGTGGTTCTCACCATTACCCAGCCCCGTTCTGAGCTTTTTCAGCTTTTGACA
-----EXON 6-----
TTGCCATCCTGAGCTTCGGAGAGCTGATTTCTGTGGCAGCCAGCGGAAATGCTTGATTTCTCAATGACTGCGGTTACCCCTGTCCTGAACATT
-----EXON 7-----
ACCCCTTTGACTTCTATATGGACCTGACGTGAGTGGATACCCAAAGCAAGGAACGGGAAATAGAAACCTCCAAGAGAGTCCAGATGATAGAATCTG
-----EXON 7-----

FIG. 14B. (1 OF 3)

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'ACAAGAAATCAGCAATTGTCAATAAACTTTGAAGATATTGAAAGAAATGAAACACCTGAAACCGTTACCAATGGTTCCCTTTCAAAACCAAGATT
-----EXON 8-----
'CTGGAGTTTCTCTAAACTGGGTGTTCTCCTGAGGAGTGACAAGAACTTGGTGAGAAATAAGCTGGCAGTGATTACGCGTCTCCTTCAGAATC
-----EXON 8-----EXON 9-----
'TCATGGGTTTGTTCCTCCTTTCTTCGTTCTGCGGGTCCGAAGCAATGTGCTAAAGGTGCTATCCAGGACCGCGTAGGTCTCCTTTACCAGTTTG
-----EXON 9-----
'GCGCCACCCCGTACACAGGCATGCTGAACGCTGTGAATCTGTTTCCCGTGCTGCGAGCTGTCAAGCGACCGAGAGTCAAGACGGCCTCTACCAGA
-----EXON 9-----EXON 10-----
'GCGAGATGATGCTGGCCTATGCACCTGCACGTCCTCCCTTCAGCGTTGTTGCCACCATGATTTTCAGCAGTGTGTGCTACTGGACGCTGGGCTTAC
-----EXON 10-----EXON 11-----
'CAAATATAGTCAACAGTGTAGTGGCTCTGCTGCCATTGCGGGGTGCTTGTGGATCTGGATTCCTCAGAAACATACAGAAATGCCCATTCCTT
-----EXON 11-----EXON 12-----
'AAATCATCAGTTATTACATTCCAAAAATATTGCAGTGAGATTCTTGTAGTCAATGAGTTCTACGGACTGAATTTCACCTTGTGGCAGCTCAAATG
-----EXON 12-----EXON 13-----
'CTGTGACAACTAATCCAATGTGTGCCTTCACTCAAGGAATTCAATTCAATTGAGAAACCTGCCCGAGGTGCAACATCTAGATTCACAATGAACCTTC
-----EXON 13-----
'TTTGTATTCAATTCAGCTCTTGTCAATCCTAGGAATAGTTGTTTTTCAAAATAAGGGATCATCTCATTAGCAGGTAGTGAAAGCCATGGCTGG
-----EXON 13-----
'AATGGAAGTGAAGCTGCCGACTGTGCATGACTGCTGAACGCTCTGAAATGAGAGTGCCATGTATTCTTTCTTGACAGGACATCTCAAGTCTTTT
-----EXON 13-----

FIG. 14B. (2 OF 3)

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CCATTAGACTCCATTGTGCCCTCTTGGATCCCAAGCAGGCCCTTGAATGCAATGGAAGTGGTTATAGTCCCTTGCTCTTACAACTTGCAGGGACATG
 -----EXON 13-----

GTATTGGAAATTGTGACTGAGCGGACCCCAAGAATGTAAATAATATTCATAAACCTATGGG
 -----EXON 13-----

EXON NUMBER	EXON SIZE	5' SPlicing SITE	3' SPlicing SITE	INTRON SIZE
1			GGTCAGgtaaggcag	-600bp
2	124	cctttaaaagCCACCGC	AGCTCAGgtaagcttg	~6kb
3	137	gccccgcagGCTCCGG	CCTGCAGgtgggcgcg	74bp
4	103	ctcctgcagAGCGACA	AAGGTGGgtgcagccc	~4kb
5	129	tgcaggtggAGGCCGT	GATCCTAgtaagtggc	~2kb
6	140	tgctggcagAGGTCA	TTTTCAGgtaagaggt	~2.5kb
7	130	tctggtcagCTCTTG	TTCTATAgtaagtgtt	~0.5kb
8	214	aacttttagTGGACCT	TCCTGAGgtaagaggc	100bp
9	206	tgttttcagGAGAGTG	AATCTGTgtaagtgcc	~1.7kb
10	139	catccccagTCCCCGT	GCTACTGgtgagggtt	~1.9kb
11	186	cttttctagGACGCTG	TCCTCAGgtaagatat	~5.3kb
12	113	tttcttaagAAACATA	ACTTGTGgtaagtatt	~1.2kb
13		ccttgacagGCAGCTC		
TOTAL				~25.9kb

NIC SEQUENCES IN CAPITAL LETTER

FIG. 14B.(3 OF 3)

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